



# ***ArrayTrack<sub>3.1.5</sub> Demonstration***

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# ArrayTrack Overview

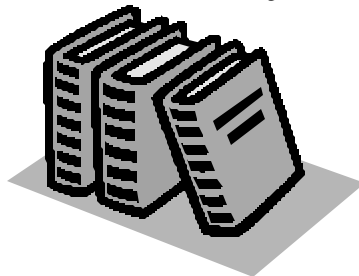
## Microarray DB



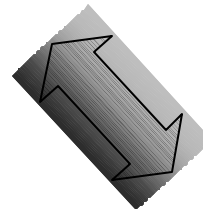
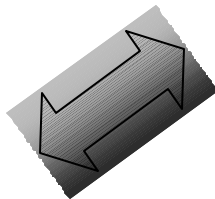
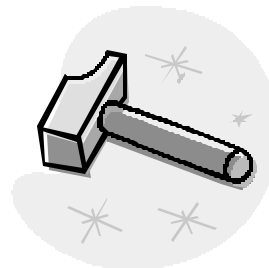
An integrated environment for microarray data management, analysis and interpretation.

Using ArrayTrack, the user can apply analysis method from Tool to microarray DB and then get Information from the linked LIB for biological interpretation

## Library

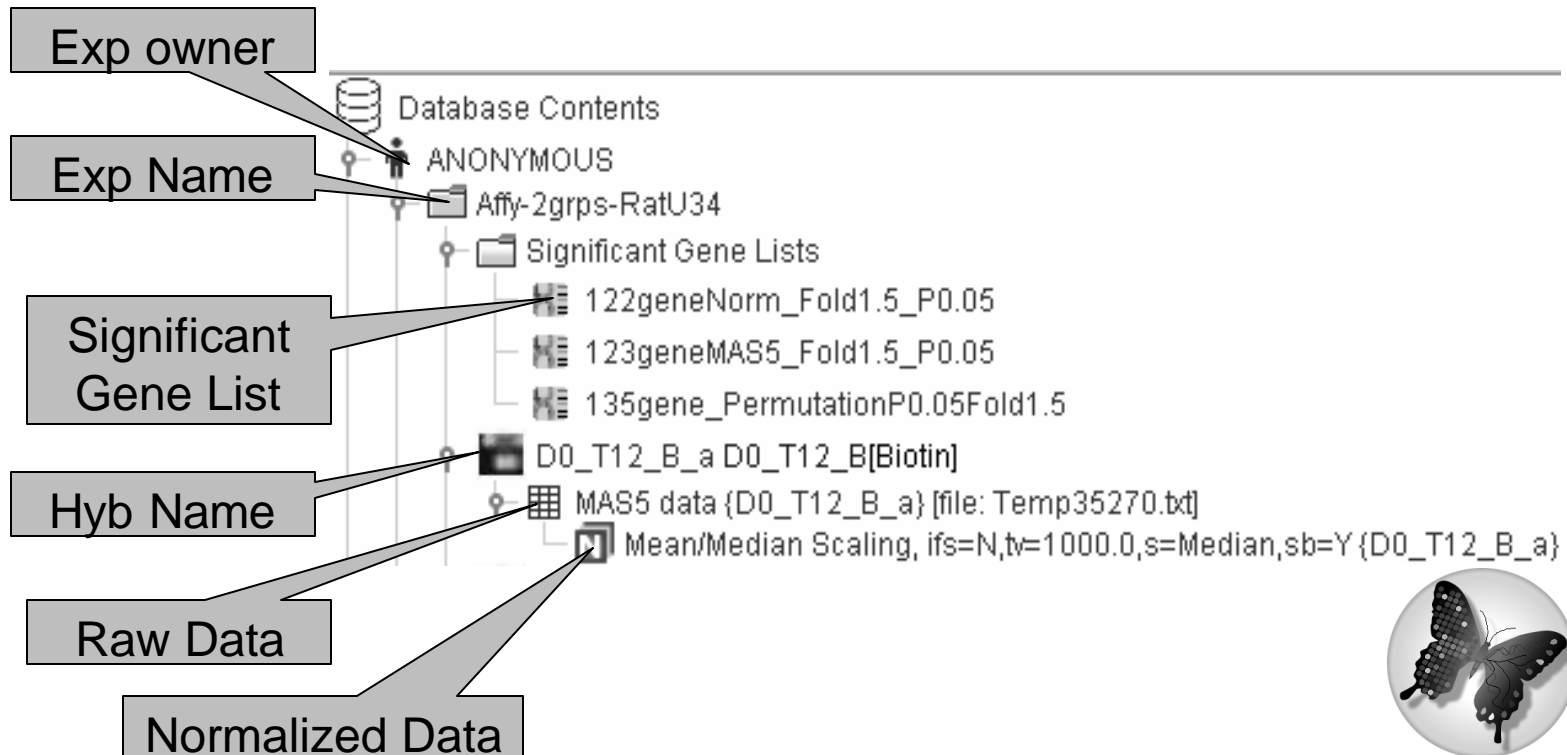


## Tool



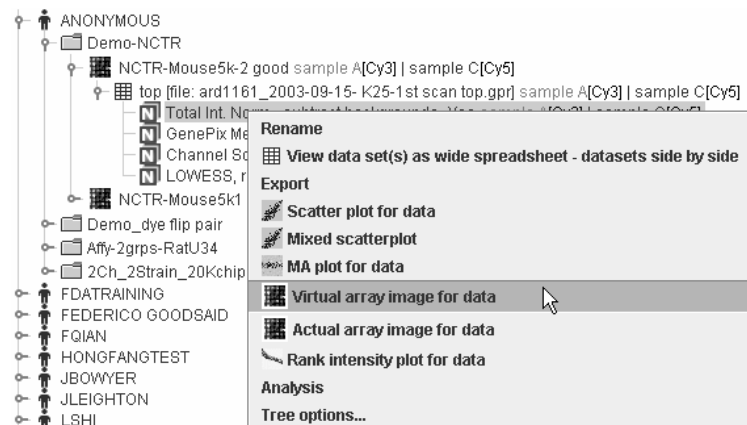
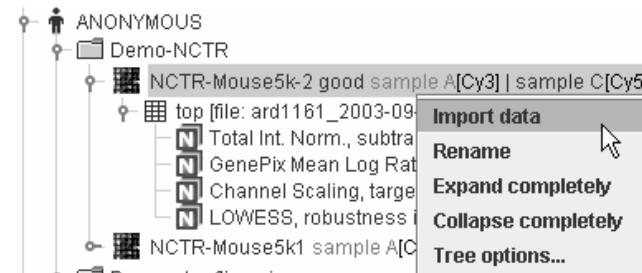
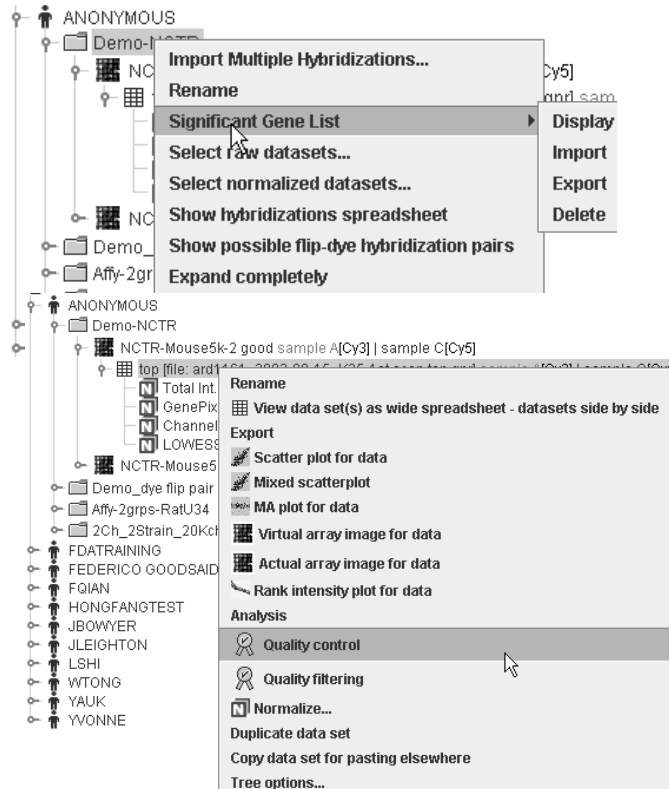
# Microarray DB

Data is organized as a hierarchical tree structure:



# Exploring DB

- Right-click exp, hybridization, raw data and normalized data to access various functions





# Importing Data



The screenshot shows the 'Input Form' window in ArrayTrack, divided into two main sections: '1 Experiment Design' and '2 Hybridization and Data'.

**1 Experiment Design**

- Experiment ID:** Demo-NCTR (with buttons for Delete Exp and Edit Privileges)
- Experiment:** anonymous, **Date:** mm/dd/yyyy (06 / 10 / 2002)
- Institute:** NCTR, **Division:** ROW
- Exp Type:** temperature shock, normal vs disease (with a Select button)
- Key words:** rat, liver, circadian
- Exp Description:** Ad lib fed rats at 6 hr. intervals, examining liver changes
- Phenotype Anchoring:** IE concentration, VITRODISE ex, core time (with a Select button)
- Comments:** (text area)
- Protocols:** Multiple fields for Import and Export buttons: Protocol, Exp Design Protocol, Hybridization Protocol, Labeling Protocol, RNA Extraction Protocol, Manuscript Reprint, Significant Gene List.
- Buttons:** Clean Form, Print Form, Help, Save Exp (with a 'Must' indicator and 'before continuing' text).

**2 Hybridization and Data**

- Hybridization:** -Select- (with Save Hyb and Delete Hyb buttons)
- Array Information:**
  - Array type:** -Select-
  - Slide ID:** (text field)
  - Array Platform:** One Channel (radio), Two Channel (radio)
  - Slide has:** 1 array(s)
  - Array used:** 1 times
- Sample & Label Information:**
  - Channel 1 / Channel 2:** (dropdowns)
  - Sample ID:** -Select- (with View/Edit button)
  - Label:** -Select- (dropdown)
  - Label by whom:** (text field)
  - When:** mm/dd/yyyy (text field)
  - OC Notes for Label:** (text area)
- Hyb Information:**
  - By whom:** (text field)
  - When:** mm/dd/yyyy (text field)
  - OC Notes for Hyb:** (text area)
- Data Import:** Import button

1. create experiment
2. create hybridization
3. create array type (if not existed in AT Chip Lib)
4. create sample

MicroarrayDB stores DNA microarray gene expression experimental data together with essential annotation information about an experiment, its protocol and the samples.

Support data from one-channel and two-channel.



# Searching Libraries



There are nine libraries in ArrayTrack.  
All the libraries are interlinked.

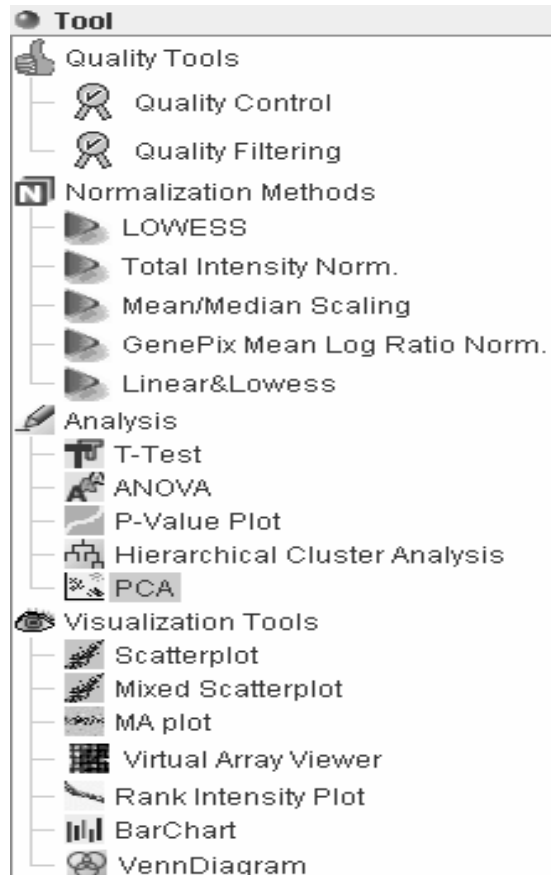
The libraries integrate gene, protein, pathway and other data allowing data interrogation and mining of data across data types.

Several ways to activate these libraries

- From library panel
- From the Library pull-down menu
- From the results of analysis (e.g. T-test)



# Analysis Tools



## Tools:

### •Quality Tools

Provides various visual plots and numerical parameters for measuring the quality of a hyb, and filtering the unwanted spots.

### •Normalization Methods

Correct systematic variations in microarray data introduced by experimental factors

### •Analysis

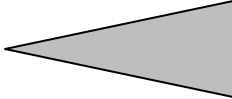
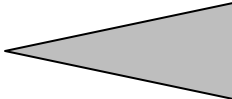
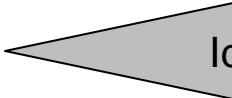
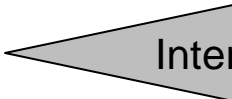
Provides different methods to evaluate the microarray data

### •Visualization Tools

Provides a direct view to identify abnormalities within data.

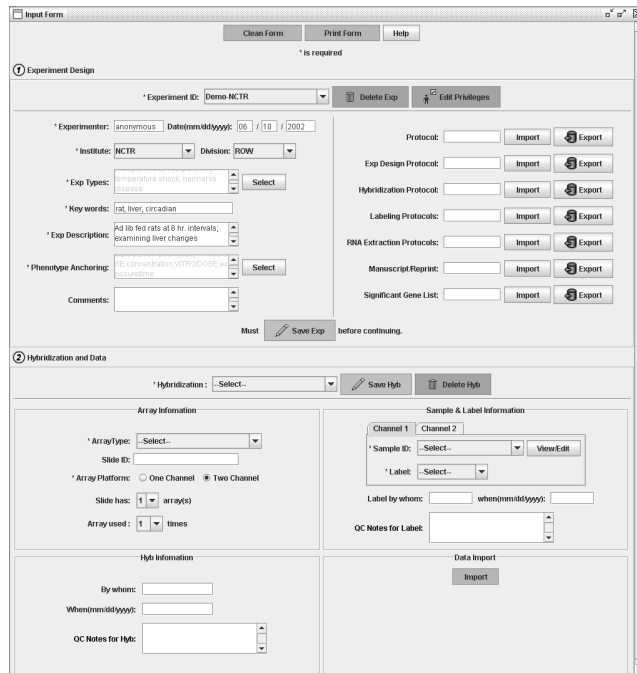
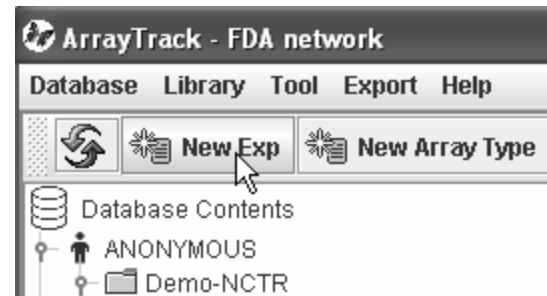


# Microarray Data Processing

- Importing data  Loading array data into AT
- Normalization  Ensure cross-chip comparison
- Gene Selection  Identify a list of significant genes
- Interpretation  Interpret data using pathways and GO



# Importing Data

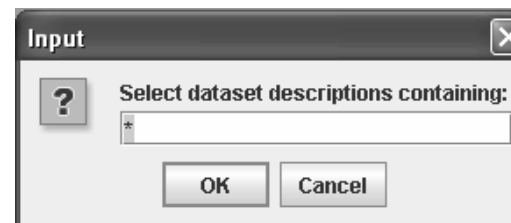
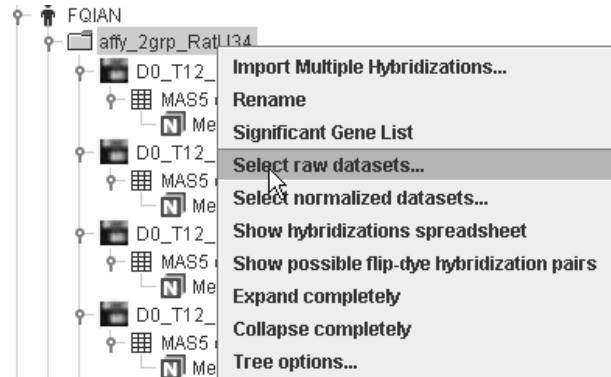
1. create experiment
2. create hybridization
3. create array type (if not existed in AT Chip LIB)
4. create sample



# Normalization

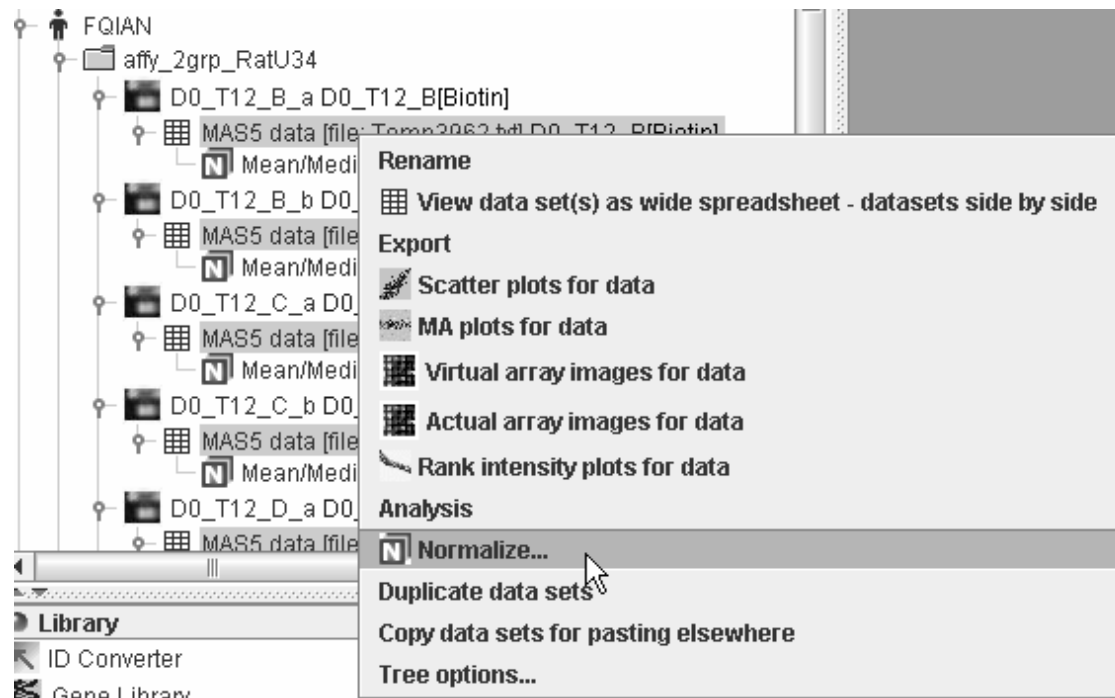
- To remove systematic variations across chips and ensure a valid cross-chip comparison

1. Right-click an experiment
2. Select “raw datasets...”



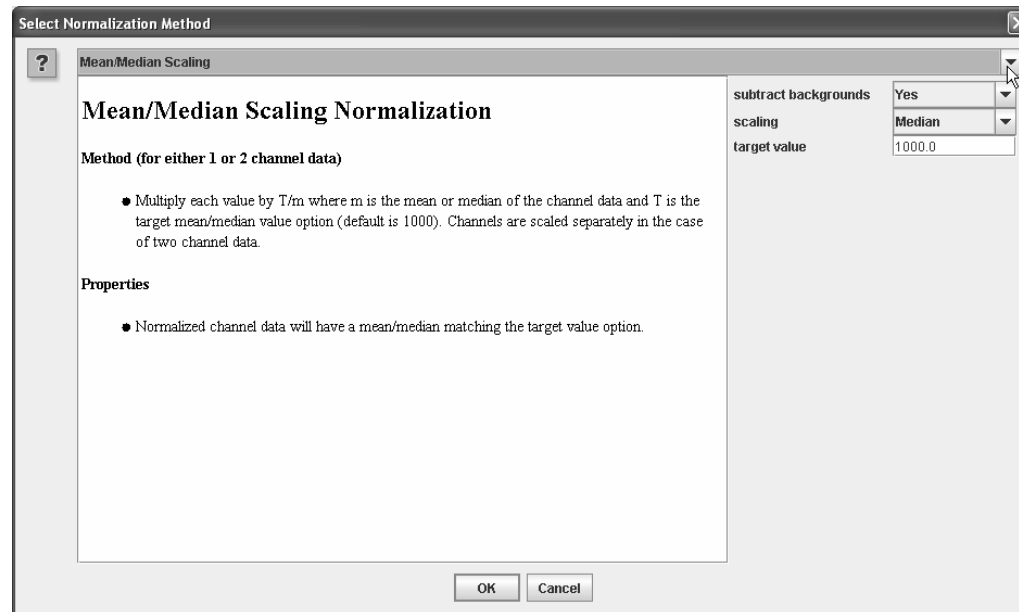
# Normalization (-continued)

3. Right-click any highlighted raw data
4. Select “Normalize...”



# Normalization (-continued)

- Choose normalization method



**Select Normalization Method**

**Mean/Median Scaling**

**Mean/Median Scaling Normalization**

Method (for either 1 or 2 channel data)

- Multiply each value by  $T/m$  where  $m$  is the mean or median of the channel data and  $T$  is the target mean/median value option (default is 1000). Channels are scaled separately in the case of two channel data.

**Properties**

- Normalized channel data will have a mean/median matching the target value option.

subtract backgrounds: Yes

scaling: Median

target value: 1000.0

OK Cancel

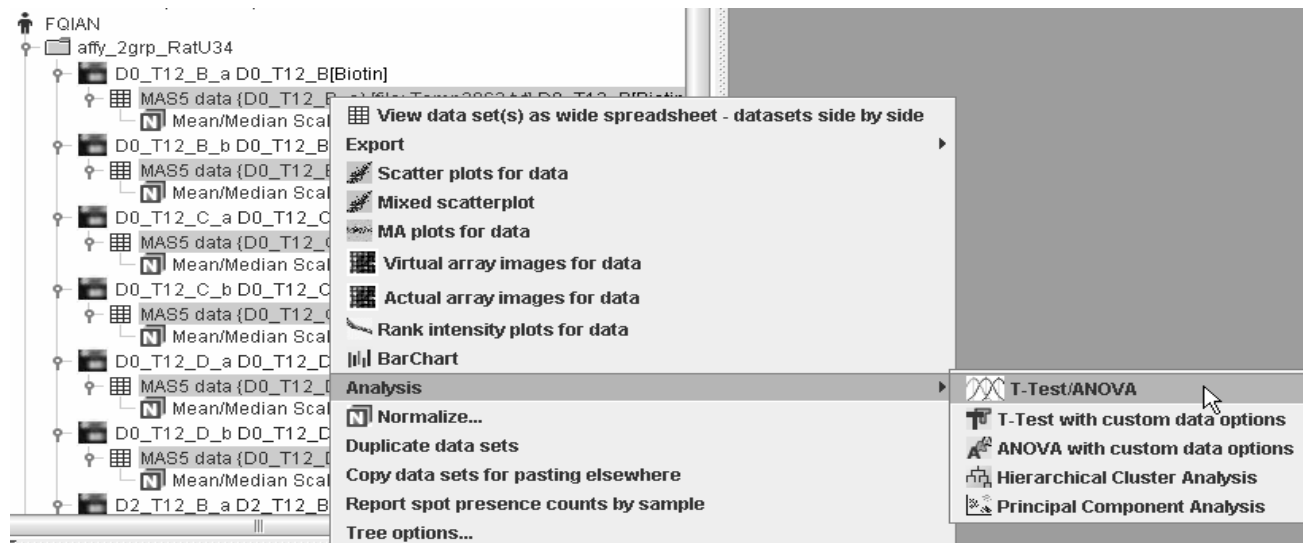
- For Affy data, choose “Mean/Median Scaling”
- For 2-channel data, the default method is “Lowess”





# Gene Selection

- Highlight and Right-click the experiment.
- Select “Normalized datasets...” and click “OK”
- Right-click the highlighted normalized data
- Choose “Analysis->T-test”



# Gene Selection (-continued)

Select Dataset Group Assignments

Edit Datasets Groups Gene Id's Data-Options

Swap Channels Groups: Assign to New Group Unassign Assign to...

	Hybridization	SAMPLE 1	LABEL 1	SAMPLE 2	LABEL 2	ARRAYNUM	SLIDE	SI
1 ①	Strain A Q380	Strain A - mice 1	Cy5	Reference	Cy3	1		1
2 ①	Strain A Q381	Strain A - mice 2	Cy5	Reference	Cy3	1		1
3 ①	Strain A Q382	Strain A - mice 3	Cy5	Reference	Cy3	1		1
4 ②	Strain B Q385	Strain B - mice 1	Cy5	Reference	Cy3	1		1
5 ②	Strain B Q386	Strain B - mice 2	Cy5	Reference	Cy3	1		1
6 ②	Strain B Q387	Strain B - mice 3	Cy5	Reference	Cy3	1		1

2 groups, sizes = [3, 3]

T-Test

T-Test Options

☒ P values from theoretical t-distribution

☒ Welch t-test ☐ Simple t-test ☐ One class vs. mean:

☐ P values from permutations of group assignments

☐ All ☒ Limit to:

Do Tests

Assign the data into 2 groups

- different dose
- different time
- or different animal



# Gene Selection (-continued)

T-Test Results							
File	Selected-Spot	All Spots					
	Genbank Acc	Gene Mfr ID	LOCUSID	GENENAME	SPOTID	P	Mean G
1	AA108277	AA108277_...	288444	na	516484	0.0001	8.507
2	AA108308	AA108308_...	314856	na	516485	0.8937	1.2235
3	AA108308	AA108308_...	314856	na	516486	0.0166	9.2682
4	AA684537	AA684537_...	294964	na	516487	0.0826	8.021
5	AA684929	AA684929_...			516488	0.1536	7.7018
6	AA684960	AA684960_...			516489	0.341	6.8608
7	AA684963	AA684963_...	293702	na	516490	0.4595	8.6452
8	AA685112	AA685112_...	293652	na	516491	0.0814	8.8775
9	AA685152	AA685152_...	25490	Nedd8	516492	0.1159	6.991
10	AA685376	AA685376_...			516493	0.346	6.558
11	AA685876	AA685876_...	304805	na	516494	0.0183	9.225
12	AA685903	AA685903_...	362862	na	516495	0.3713	11.1139
13	AA686031	AA686031_...	301458	na	516496	0.1077	7.0271
14	AA686579	AA686579_...	301442	na	516497	0.9527	5.0000
15	AA686870	AA686870_...			516498	0.308	6.507
16	AA686870	AA686870_...			516499	0.0001	3.3942
17	AA799336	AA799336_...	293453	na	516500	0.6183	9.8132

1031 genes

Significance Filtering

☒ P Values < 0.05 without adjustment

☐ Select # genes: lowest p-vals

Mean Channel Intensities > Bad Flags <=

Fold Change > 2

Apply Filters

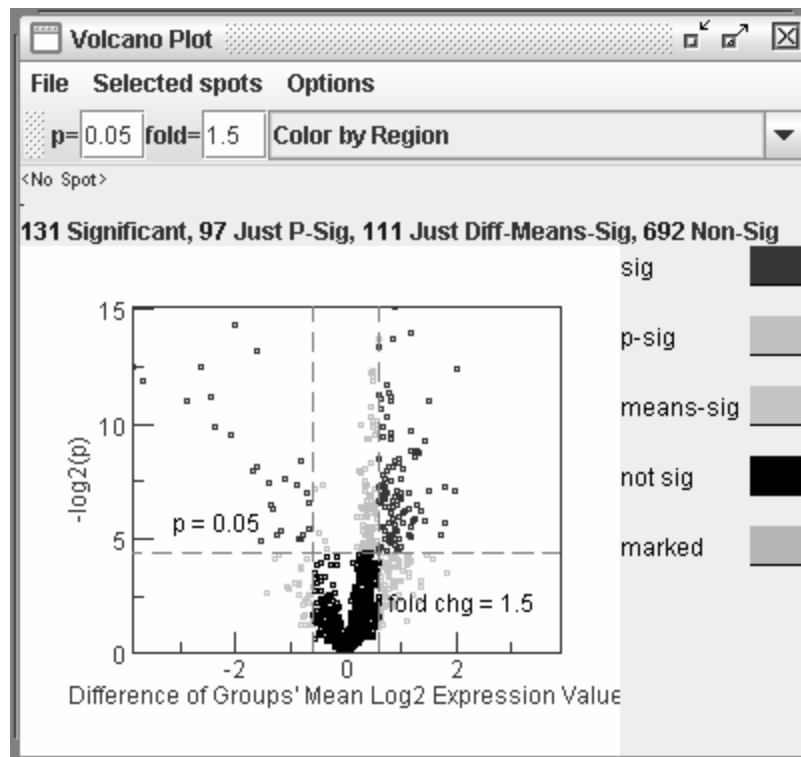
P-Value Plot Create Sig. Gene List HCA PCA Volcano Plot

Parameters used to filter the genes to get significant gene list

Access other analysis methods like HCA, PCA, Volcano plot, etc.



# Gene Selection (-continued)



Volcano Plot



# Significant Gene List

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- Create
- Display
- Import
- Export
- Delete

# Significant Gene List(-cont)

- Create significant gene list

From T-test/Anova result

set filter criteria

e.g. P-value, fold change

to get significant gene list

Create significant gene list

Filter criteria

The screenshot shows the 'T-Test Results' software window. The main table lists genes with columns for Genbank Acc, SPOTID, (1) P, Mean Grp 1, Mean Grp 2, and Fold Change. A callout box points to the 'Create significant gene list...' option in the 'All Spots' menu. Another callout box points to the 'Filter criteria' section in the bottom panel, which includes options for P-values, FDR, and fold change.

Genbank Acc	SPOTID	(1) P	Mean Grp 1	Mean Grp 2	Fold Change
NM_013474	149926	0	6.4884	2.7783	13.0868
AY065541	146938	0	-2.0418	-3.7955	3.3721
AK013100	151257	0.0001	-1.5408	-0.7993	0.5981
U86105	150780	0.0007	-0.2051	-0.5849	1.3012
NM_021304	159805	0.0008	-3.0816	1.5725	0.0397
U86105	159805	0.0008	0.9588	-0.7275	3.2184
AK018313	156273	0.0011	-0.6934	1.1372	0.2812
NM_008865	150780	0.0007	0.242	0.0395	1.1507
NM_008865	159805	0.0008	-0.8595	-1.748	1.8513
NM_019486	162758	0.0008	0.2548	-0.0529	1.2377
NM_008319	145874	0.0009	-0.1589	-0.4882	1.2564
NM_021447	149205	0.001	0.4095	0.1626	1.1867
NM_015780	148342	0.0011	1.2908	3.2995	0.2485
D43759	156273	0.0011	5.9168	4.6198	2.4571
NM_010419	157161	0.0011	0.3868	0.1695	1.1625
AF331708	158777	0.0012	-1.6946	0.4169	0.2314
AB041350	158418	0.0012	-2.8198	-3.7082	1.8511

20160 genes

Significance Filtering

☒ P Values <  without adjustment

☐ Target False Discovery Rate (FDR):

☐ Select # genes with lowest p-vals:

Mean Channel Intensities >  Bad Flags <=

Fold Change >

Apply Filters

P-Value Plot MAQC Create Sig. Gene List HCA PCA Volcano Plot

# Significant Gene List(-cont)

- **Display/Import/Export/Delete Significant Gene List**

Right-click the experiment name

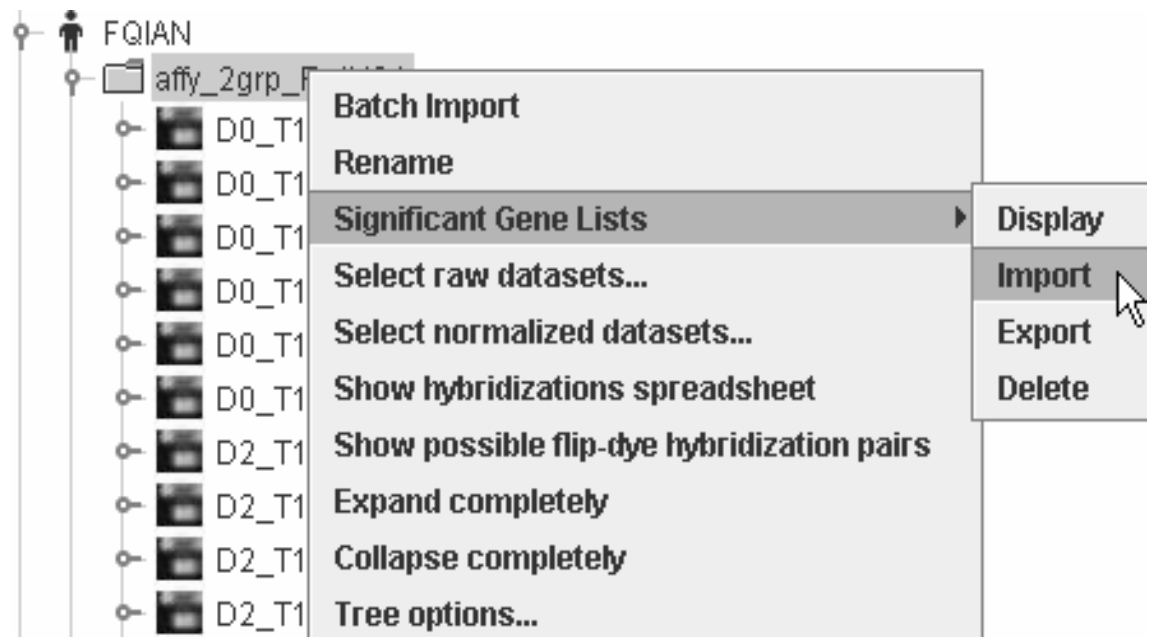
select Significant Gene Lists

select Display

Import

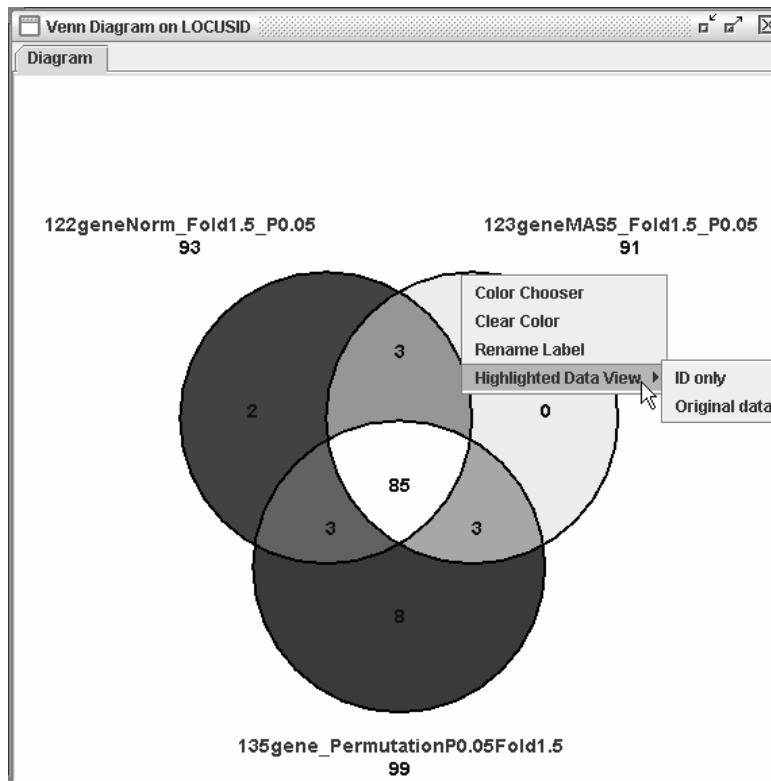
Export

Delete



# Significant Gene List(-cont)

- **VennDiagram** - get common genes from 2~3 significant gene lists



Visualization Tools

- Scatterplot
- Mixed Scatterplot
- MA plot
- Virtual Array Viewer
- Rank Intensity Plot
- BarChart
- VennDiagram

New Exp New Array Type

Significant Gene Lists

- 1991withSwissprot\_Pro
- Locus\_ID\_5pathway\_G
- D0\_T12\_B\_a D0\_T12\_B[Bi
- MAS5 data {D0\_T12\_B\_
- D0\_T12\_B\_b D0\_T12\_B[Bi
- MAS5 {D0\_T12\_B\_b} file

EPA  
FDATRaining  
FEDERICO GOODSaid  
FQIAN

Open  
Export  
Rename  
Delete  
VennDiagram

Manufacture ID  
Locus ID  
Spot ID  
by Pathway

Tool Export Help

Visualizations

- Virtual Array Viewer
- Scatter Plot
- Mixed Scatterplot
- MA Plot
- Rank Intensity Plot

Quality-Control

Normalization

Analysis

Preferences...

Convert Affy cel file to expression

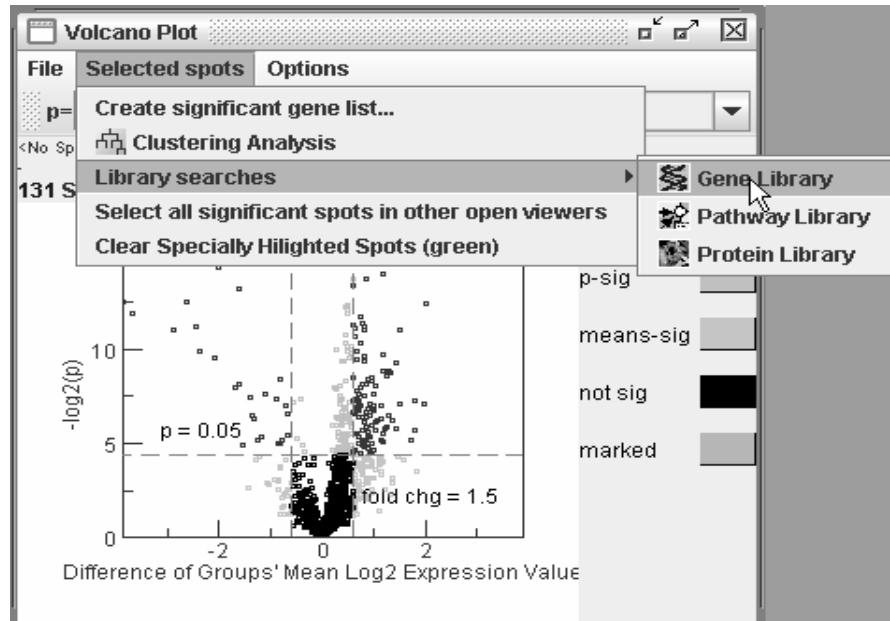
Split File By Columns

Cross-Dataset Gene Barchart...

VennDiagram



# Interpretation



Link the significant genes to Gene Library for data interpretation



# Interpretation (continued)

Gene Library

1 Specify ID Type:

☐ GenBankAcc

☐ UnigenelD

☐ LocusID

☐ SwissProtAcc

☐ IMAGEID

☐ GEN\_ID\_MFR

☐ GeneSymbol

☒ Hs ☐ Mm ☐ Rn

2 Enter Searching Data:

3 Search ☐ within result

Clear

Message:  
unique search ID number :94

	GENENAME	DESCRIPTION	SPECIES	CHROMLOCA.	LOCUSID	BIOLOGI
1	Nat1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	Rattus norvegicus	16p14	116631	metabolism
2	Tap1	transporter 1, ATP-binding cassette, subfamily S	Rattus norvegicus	20p12	24811	defense response;immune response
3	Mef2d	myocyte enhancer factor 2D	Rattus norvegicus	2q34	81518	
4	Adprt	ADP-ribosyltransferase 1	Rattus norvegicus	13q26	25591	protein amino acid ADP-ribosylation
5	Dpyd	dihydropyrimidine dehydrogenase	Rattus norvegicus	2q41	81656	pyrimidine base catabolism
6	Mapk7	mitogen-activated protein kinase 7	Rattus norvegicus	10q23	114509	
7	LOC288591	similar to transmembrane protein inducible by	Rattus norvegicus	12q12	288591	
8	Dusp6	dual specificity phosphatase 6	Rattus norvegicus	7q13	116663	cell differentiation;protein amino acid metabolism
9	LOC288444	similar to heat shock protein 105 kDa	Rattus norvegicus	12p11	288444	
10	Gstm5	glutathione S-transferase, mu 5	Rattus norvegicus	2q34	64352	
11	Nras	neuroblastoma RAS viral (v-ras) oncogene	Rattus norvegicus	2q34	24605	Ras protein signal transduction;cell growth
12	Rara	retinoic acid receptor, alpha	Rattus norvegicus	10q31	24705	regulation of anti-apoptosis;regulation of cell death
13	Dia1	diaphorase 1	Rattus norvegicus	7q34	25035	electron transport
14	Cd44	CD44 antigen	Rattus norvegicus	3q31	25406	cell adhesion;defense response;cell growth
15	Nat2	N-Acetyltransferase-2	Rattus norvegicus	16p14	116632	metabolism
16	LOC308047	similar to heat shock protein, DNAJ-like	Rattus norvegicus	1p11	308047	
17	Met	met proto-oncogene	Rattus norvegicus	4q21	24553	adult behavior;brain development
18	Hspb1	heat shock 27kDa protein 1	Rattus norvegicus	12q12	24471	
19	Mapk14	mitogen activated protein kinase 14	Rattus norvegicus	20p12	81649	angiogenesis;protein amino acid metabolism
20	LOC363249	similar to golli-interacting protein	Rattus norvegicus	9q33	363249	
21	Hadha	hydroxyacyl-Coenzyme A dehydrogenase	Rattus norvegicus	6q12	170670	fatty acid metabolism;metabolism
22	Camlg	calcium modulating ligand	Rattus norvegicus	17p14	81715	
23	Cdk7	cyclin-dependent kinase 7 (MO15 homolog)	Rattus norvegicus	2q12	171150	cell cycle;cell cycle;cytokinesis;mitosis
24	Cox6a2	cytochrome c oxidase, subunit VIa, polypeptide	Rattus norvegicus	11q36	25278	electron transport
25	Mt1a	Metallothionein	Rattus norvegicus	19p12	24567	nitric oxide mediated signal transduction
26	Hspa1b	heat shock 70kD protein 1B	Rattus norvegicus	20p12	294254	response to heat
27	LOC293991	similar to NADH dehydrogenase (ubiquinone)	Rattus norvegicus	1q54	293991	
28	LOC315994	similar to Expressed sequence A18746	Rattus norvegicus	8q32	315994	
29	Map3k1	mitogen activated protein kinase kinase	Rattus norvegicus	2q14	116667	protein amino acid phosphorylation

•The significant genes are listed here in Gene Library.

•Can search and sort the Gene library

•There are links to other Libraries(Kegg, Pathart)



# Interpretation (continued)

- KEGG – Kyoto Encyclopedia of Genes and Genomes  
<http://www.genome.jp/kegg/>
- KEGG is a suite of databases and associated software.
- KEGG Pathway database provides the information of metabolic, regulatory and disease pathways; Most of them are metabolic pathways.



# Interpretation (continued)

PathArt (Jubilant) – a pathway database

- The Pathways (over 600 mammalian disease and signaling)
- The Pathways is a collection of manually curated information from literature and public domain databases.

## In ArrayTrack

	Human	Rat	Mouse
Kegg	134	116	124
PathArt	587	151	297



# Interpretation (continued) Kegg

Gene	Map	Category	Fisher P Value
Gstm5 Gpx1	Glutathione metabolism(mmu00480)	Metabolism of Other Amino Acids/Metab...	0.00370292
Ptgs2	Prostaglandin and leukotriene metaboli...	Lipid Metabolism/Metabolic pathway	0.25805128
Hmox1	Porphyrin and chlorophyll metabolism(m...	Metabolism of Cofactors and Vitamins/M...	0.13404114
Dusp6 Hspb1 Mapk7 Mapk14 Tnfrsf1a Tgfb2 Nras Mapk9 Map3k1	MAPK signaling pathway(mmu04010)	Regulatory pathway	0.00019113
Met Ngfr Tgfb2 Tnfrsf1a	Cytokine-cytokine receptor interaction(m...	Regulatory pathway	0.17855902
Tnfrsf1a	Apoptosis(mmu04210)	Regulatory pathway	0.58437738
Mapk9	Wnt signaling pathway(mmu04310)	Regulatory pathway	0.77999365
Tgfb2	TGF-beta signaling pathway(mmu04350)	Regulatory pathway	0.55443832
Mapk14 Mapk9	Toll-like receptor signaling pathway(mm...	Regulatory pathway	0.23520864
Csnk1d	Circadian rhythm(mmu04710)	Regulatory pathway	0.11721566
Mapk14 Mapk9	Parkinson's disease(mmu05020)	Regulatory pathway	0.03611750
Gpx1	Amyotrophic lateral sclerosis (ALS)(mm...	Regulatory pathway	0.15056025

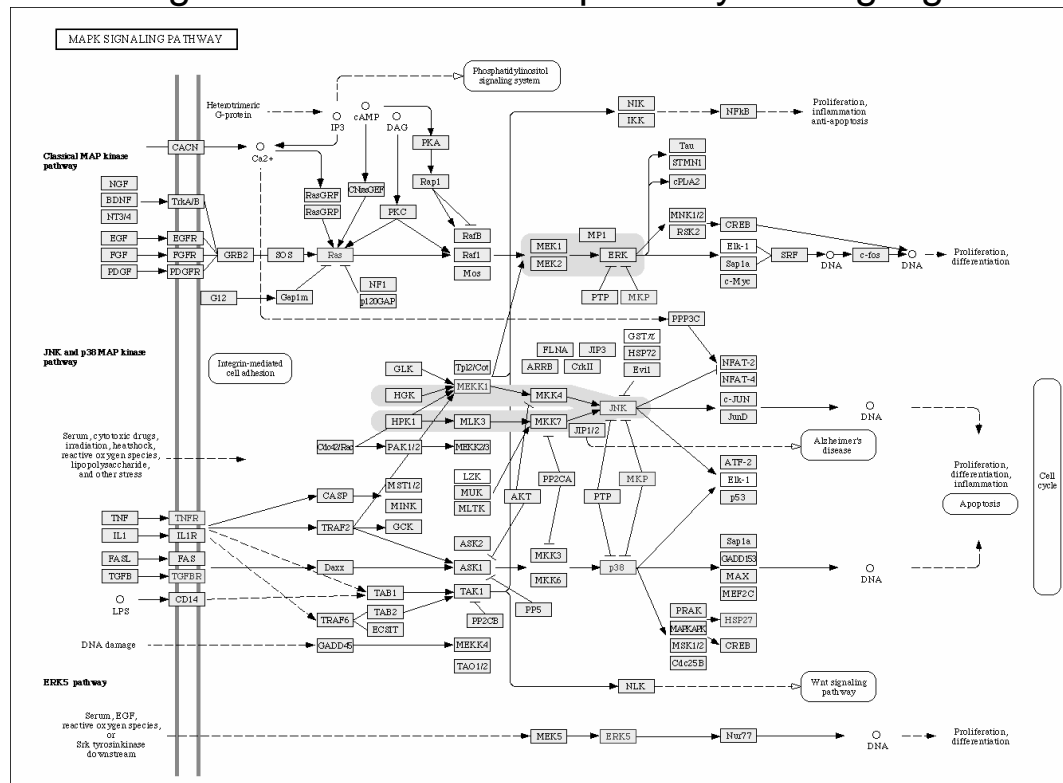
Input genes = 60, 22 genes found, 38 not found, Total 23 pathway maps.

Kegg Pathway



# Interpretation (continued) Kegg

Double-click a specific pathway, the pathway map will be displayed and the genes involved in the pathway are highlighted.



# Interpretation (continued) PathArt

Genes

Pathways

Physiology/disease

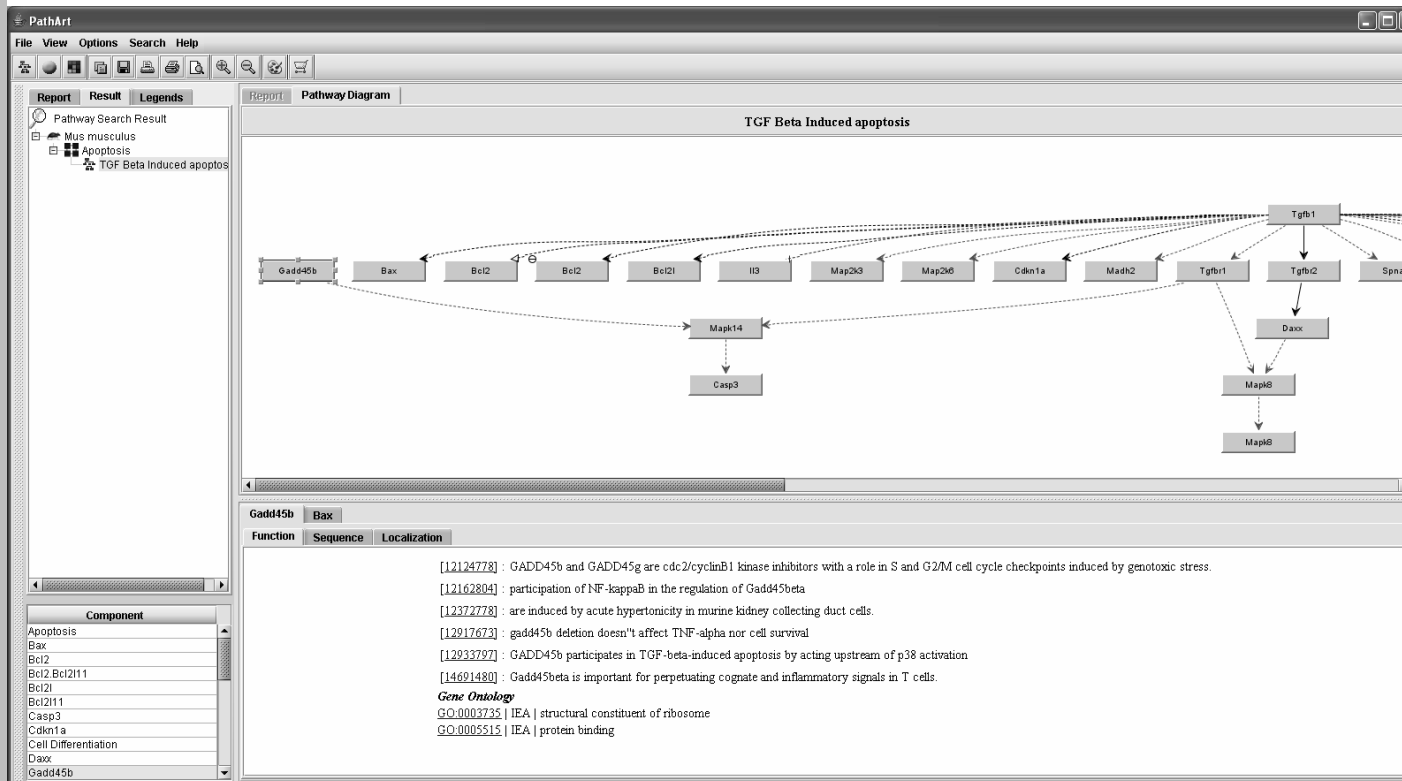
Statistical  
significance of the  
pathway

Component n...	Pathway Name	Organism	Physiology/...	IS_PHYSIO...	Pathway Ty...	Fisher P V...
Mapk14	CCR5 Mediated Pathway	Mus muscu...	Acquired I...	Disease	Signaling	0.089682
Gc1c	Tat Signaling Pathway	Mus muscu...	Acquired I...	Disease	Signaling	0.236507
Mapk14	AGEs Signaling Pathway	Mus muscu...	Alzheimers	Disease	Signaling	0.149045
Mapk14	Amyloidbeta-peptide Signal...	Mus muscu...	Alzheimers	Disease	Signaling	0.118019
Tnfrsf1a	IFN Signaling Pathway	Mus muscu...	Alzheimers	Disease	Signaling	0.634464
Mapk14	LPS Signaling Pathway	Mus muscu...	Alzheimers	Disease	Signaling	0.386674
Map3k1	DR4/5 Signaling Pathway	Mus muscu...	Apoptosis	Physiology	Signaling	0.064863
Mapk14	IGF Signaling Pathway	Mus muscu...	Apoptosis	Physiology	Signaling	0.717471
Ngfr	NGF Signaling Pathway	Mus muscu...	Apoptosis	Physiology	Signaling	0.204750
Mef2d	T-cell apoptosis	Mus muscu...	Apoptosis	Physiology	Signaling	0.149045
Mapk14	TGF Beta Induced apoptosis	Mus muscu...	Apoptosis	Physiology	Signaling	0.051402
Tgfr2	TGF Beta Induced apoptosis	Mus muscu...	Apoptosis	Physiology	Signaling	0.051402
Tnfrsf1a	TNF Signaling Pathway	Mus muscu...	Apoptosis	Physiology	Signaling	0.776034
Mapk14	TNFR1 Signaling Pathway	Mus muscu...	Apoptosis	Physiology	Signaling	0.246824
Adprt	TRAIL Mediated Apoptosis	Mus muscu...	Apoptosis	Physiology	Signaling	0.378170
Mapk14	UV induced Antiapoptotic P...	Mus muscu...	Apoptosis	Physiology	Signaling	0.113880
Cd44	WNT Signaling Pathway	Mus muscu...	Apoptosis	Physiology	Signaling	0.644709
Mapk14	Interleukin Signaling Pathw...	Mus muscu...	Atheroscle...	Disease	Signaling	0.926753
Met	HGF Signaling Pathway	Mus muscu...	Breast Ca...	Disease	Signaling	0.064863
Tgfr2	TGF Signaling Pathway	Mus muscu...	Breast Ca...	Disease	Signaling	0.267067
Cd44	CD44 Signaling Pathway	Mus muscu...	Cell Adhe...	Physiology	Signaling	0.052216
Tp53	ATR-ATM Signaling Pathway	Mus muscu...	Cell Cycle	Physiology	Signaling	0.204750
Map3k1	Bcr-Abl Signaling Pathway	Mus muscu...	Chronic M...	Disease	Signaling	0.217718
Vegf	Bcr-Abl Signaling Pathway	Mus muscu...	Chronic M...	Disease	Signaling	0.217718

Total genes = 60, Found genes = 17, Found pathways = 58



# Interpretation (continued) PathArt





# Interpretation (continued) GOFFA

- Developed based on Gene Ontology(GO) database
- Grouping the genes into functional classes
- GO- three ontologies
  - Molecular function: activities performed by individual gene products at the molecular level, such as catalytic activity, transporter activity, binding.
  - Biological process: broad biological goals accomplished by ordered assemblies of molecular functions, such as cell growth, signal transduction, metabolism.
  - Cellular component: the place in the cell where a gene product is found, such as nucleus, ribosome, proteasome.



# Interpretation (continued)

## GOFFA

**Go Term Cluster**

Select data type

☐ GenBankAcc

☐ UnigenID

☐ LocusID

☐ SwissProtAcc

☒ GeneSymbol

☐ Protein ID

Select genome

☐ Human ☒ Mouse ☐ Rat

Input Data

LOC288444  
GJB3  
MAPK14  
RARA  
HADHA  
MEF2D  
HMOX1  
MET  
NAT2  
NGFR  
ADPR  
LOC288727  
LOC308047  
BACH  
CYP2C13  
LOC293991  
COX6A2  
CAMLG  
PTGS2  
CRYAB  
DNAJA1  
MAP3K1  
HSPB1  
HSPB1

Search GO

Total submit =60, Found =49

**Tree** Term Clustering All Genes P Path Plot

all(49 P=1.000000)

- biological\_process(47 P=0.002730)
  - development(14 P=0.004792)
    - morphogenesis(9 P=0.039353)
      - organogenesis(8 P=0.045786)
        - tube morphogenesis(1 P=0.137460)
        - cellular morphogenesis(1 P=0.546747)
        - embryonic morphogenesis(2 P=0.054143)
      - embryonic development(2 P=0.179509)
      - reproduction(3 P=0.059708)
      - cell differentiation(1 P=0.794819)
      - growth(1 P=0.379243)
      - pigmentation(1 P=0.146151)
      - regulation of development(1 P=0.449401)
        - mesoderm development(1 P=0.159028)
    - physiological process(41 P=0.010023)
    - behavior(2 P=0.114910)
    - cellular process(23 P=0.582550)
    - regulation of biological process(12 P=0.128288)
  - molecular\_function(46 P=0.122915)
  - cellular\_component(29 P=0.999926)
    - extracellular(10 P=0.353575)
      - extracellular space(10 P=0.235583)
    - cell(24 P=0.998997)
    - organelle(10 P=0.991753)
    - protein complex(7 P=0.304521)

Search in Tree

Find terms containing

☒ GO term ☐ Gene name or gene symbol ☐ P Value

Search Clear

NO	Gene Products
1	NME6
2	CYP1A1
3	PTGS2
4	NGFR
5	DAO1
6	TAP1
7	TNFRSF1A
8	COX6A2
9	MET
10	VEGF

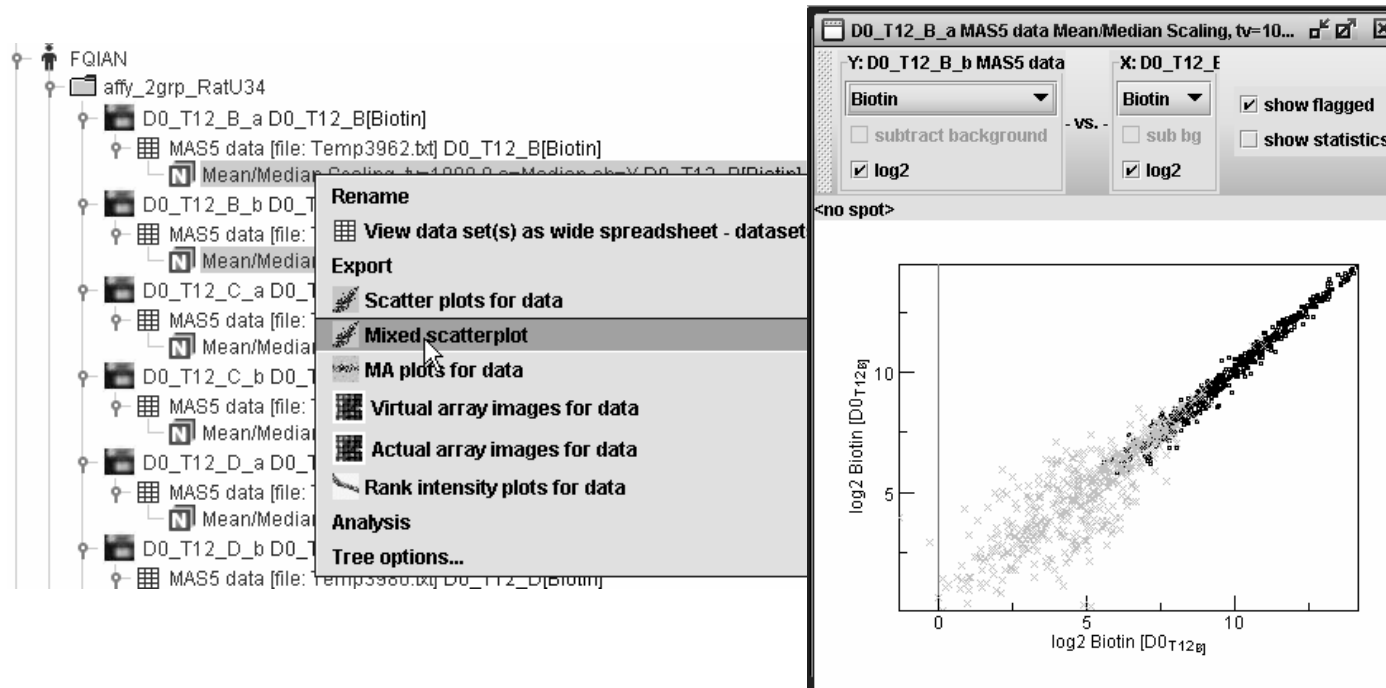


# Data Exploring

- **Scatter Plot**  
plot the fluorescence intensity data of Cy3 vs Cy5 for the same array
- **Mixed Scatter Plot**  
compare two arrays in one plot, applies to both 2-channel and 1-channel data.
- **Principal Component Analysis (PCA)**  
PCA is a way of identifying the data patterns and highlighting the data's similarity and difference.
- **Bar Chart**  
displays expression data for a single gene across multiple arrays within the same experiment or across different experiment.
- **HCA**  
is comprised of agglomerative methods and divisive methods that finds clusters of observations within a data set.

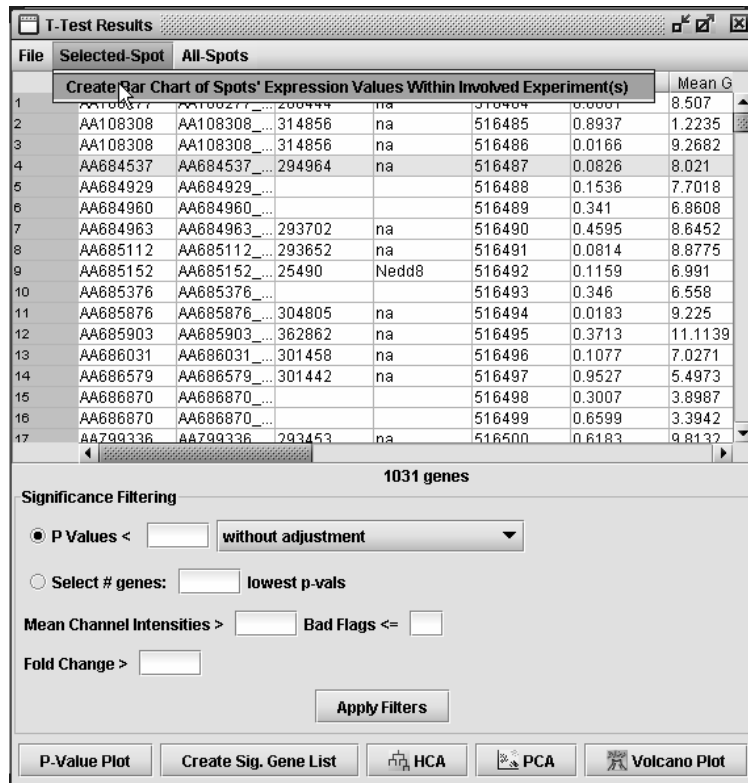


# Data Exploring scatter plot



# Data Exploring

## Bar chart



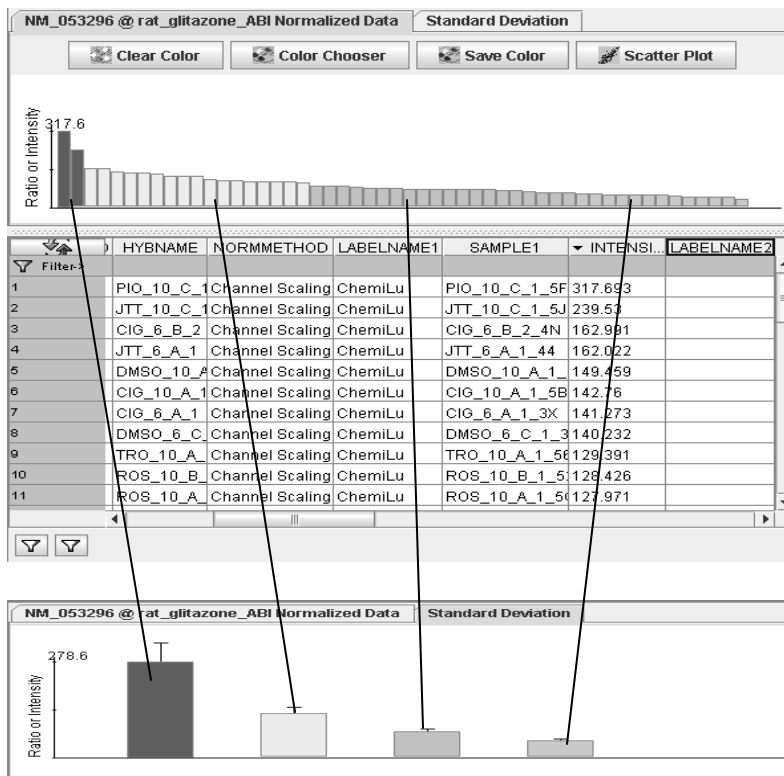
Access Bar chart from T-Test results.

Bar chart – display expression data for a single gene across multiple arrays in the same experiment or across different experiments.



# Data Exploring

## Bar chart continued



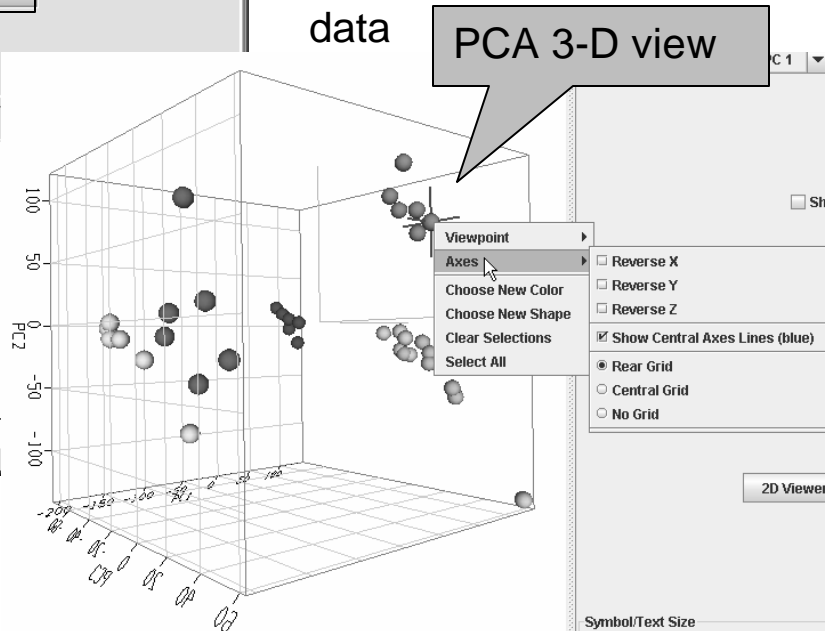
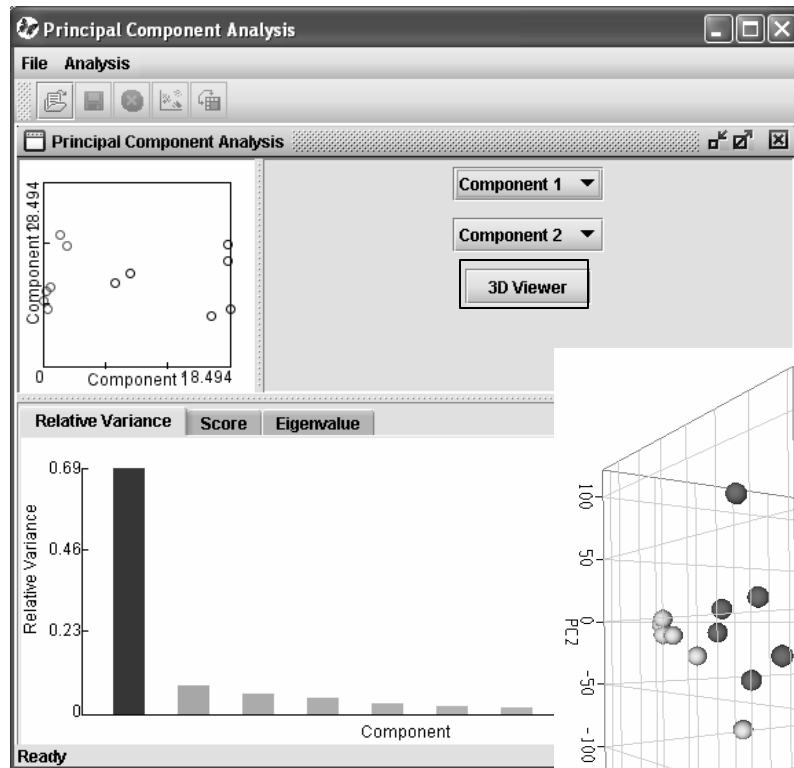
Grouping multiple arrays marked in different colors

Standard deviation bar chart for the above groups. The bar height represents the mean intensity, while the T-line above the bar stands for the value of SD. The color for each bar echoes the color of the bar chart at the top, in the same order.



# Data Exploring PCA

- Commonly used before gene selection
- To investigate the inter-sample relationship based on the gene expression profile
- Identify the biological/technical replicates
- View the variance of a multidimensional data







# Accessing ArrayTrack

- FDA Internal:  
<http://weblaunch.nctr.fda.gov/jnlp/arraytrack/index.html>  
<http://weblaunch.nctr.fda.gov/jnlp/arraytrack/citrix/index.html>
- FDA External:  
<http://edkb.fda.gov/webstart/arraytrack/index.html>



# Technical Support

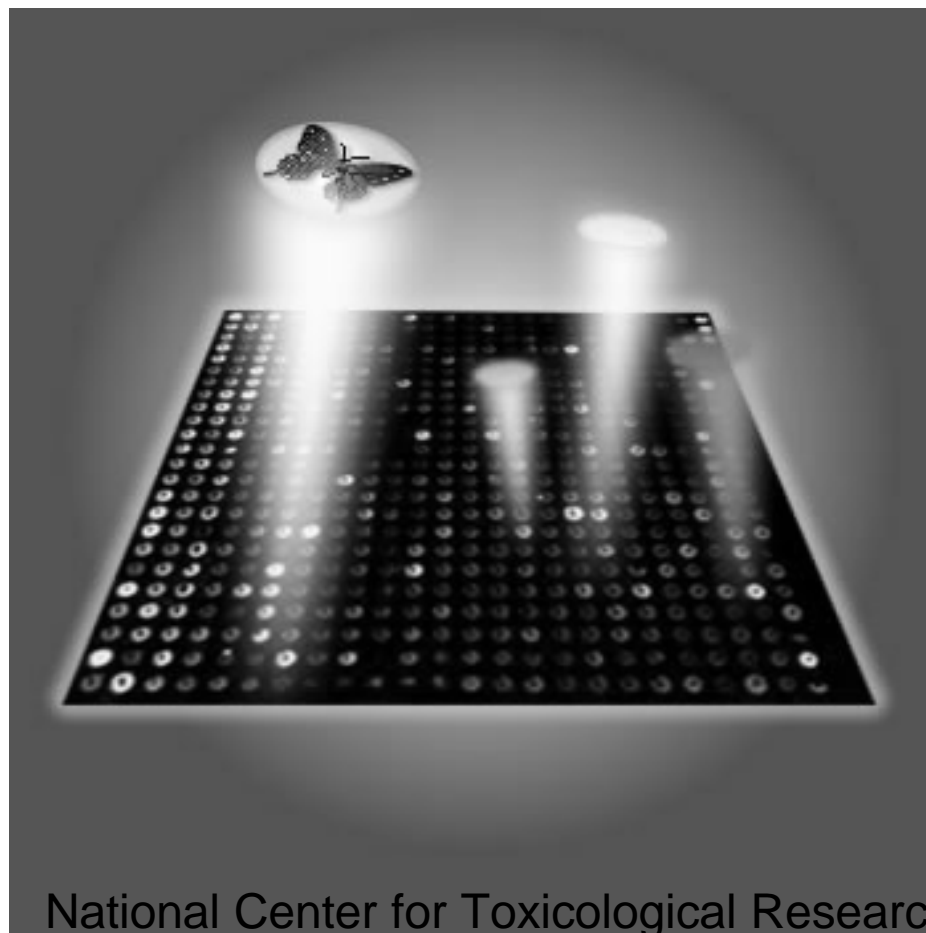
[NCTRBioinformaticsSupport@nctr.fda.gov](mailto:NCTRBioinformaticsSupport@nctr.fda.gov)

ArrayTrack is developed by the U.S. Food and Drug Administration, National Center for Toxicological Research (FDA/NCTR).

FDA/NCTR reserves all rights for the software .



# Thank you!



National Center for Toxicological Research  
U.S. Food and Drug Administration